

CRF Errors Corrected by the STIC System, Branch

C/PE

Serial Number: 10/059,720

CRF Processing Date: 3/7/2002
 Edited by: AN
 Verified by: AN (STIC staff)

E T

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: _____
- ☒ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically: _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically: _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted **ending** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☐ Other: _____

***Examiner:** The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

RAW SEQUENCE LISTING

DATE: 03/07/2002

PATENT APPLICATION: US/10/059,720

TIME: 18:53:34

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF3\03072002\J059720.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: VINSON, Charles R.

7 KRYLOV, Dmitry

9 (ii) TITLE OF INVENTION: EXTENSION OF A PROTEIN-PROTEIN

10 INTERACTION SURFACE TO INACTIVATE THE FUNCTION OF A

11 CELLULAR PROTEIN

13 (iii) NUMBER OF SEQUENCES: 64

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: MORGAN & FINNEGAN, L.L.P.

17 (B) STREET: 345 Park Avenue

18 (C) CITY: New York

19 (D) STATE: NY

20 (E) COUNTRY: USA

21 (F) ZIP: 10154-0053

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: MS WORD 97

27 (D) SOFTWARE: ASCII

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: US/10/059,720

C--> 31 (B) FILING DATE: 29-Jan-2002

41 (vii) PRIOR APPLICATION DATA:

34 (A) APPLICATION NUMBER: 60/001,654

35 (B) FILING DATE: 31-JUL-1995

38 (A) APPLICATION NUMBER: 60/018,496

39 (B) FILING DATE: 29-MAY-1996

42 (A) APPLICATION NUMBER: 08/690,011

43 (B) FILING DATE: 31-JULY-1996

45 (viii) ATTORNEY/AGENT INFORMATION:

46 (A) NAME: Serunian, Leslie A.

47 (B) REGISTRATION NUMBER: 35,353

48 (C) REFERENCE/DOCKET NUMBER: 2026-4199US2

50 (ix) TELECOMMUNICATION INFORMATION:

51 (A) TELEPHONE: (212)758-4800

52 (B) TELEFAX: (212)751-6849

54 (2) INFORMATION FOR SEQ ID NO: 1:

56 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 24 amino acids

58 (B) TYPE: amino acid

59 (C) STRANDEDNESS: unknown

60 (D) TOPOLOGY: linear

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```

62      (ii) MOLECULE TYPE: peptide
64      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
67 Asp Pro Asp Leu Glu Lys Glu Ala Glu Glu Leu Glu
68 1          5          10
70 Gln Glu Asn Ala Glu Leu Glu Leu Glu Asp Ser Phe
71          15          20
74 (2) INFORMATION FOR SEQ ID NO: 2:
76      (i) SEQUENCE CHARACTERISTICS:
77          (A) LENGTH: 25 amino acids
78          (B) TYPE: amino acid
79          (C) STRANDEDNESS: unknown
80          (D) TOPOLOGY: linear
82      (ii) MOLECULE TYPE: peptide
84      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
87 Asp Pro Asp Leu Glu Lys Glu Ala Glu Glu Leu Glu
88 1          5          10
90 Gln Glu Asn Ala Glu Leu Glu Glu Leu Glu Asp Ser
91          15          20
93 Phe
94 25
98 (2) INFORMATION FOR SEQ ID NO: 3:
100     (i) SEQUENCE CHARACTERISTICS:
101         (A) LENGTH: 26 amino acids
102         (B) TYPE: amino acid
103         (C) STRANDEDNESS: unknown
104         (D) TOPOLOGY: linear
106     (ii) MOLECULE TYPE: peptide
108     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
111 Asp Pro Asp Leu Glu Lys Glu Ala Glu Glu Leu Glu
112 1          5          10
114 Gln Glu Asn Ala Glu Leu Glu Glu Glu Leu Glu Asp
115          15          20
117 Ser Phe
118 25
121 (2) INFORMATION FOR SEQ ID NO: 4:
123     (i) SEQUENCE CHARACTERISTICS:
124         (A) LENGTH: 19 amino acids
125         (B) TYPE: amino acid
126         (C) STRANDEDNESS: unknown
127         (D) TOPOLOGY: linear
129     (ii) MOLECULE TYPE: peptide
131     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
134 Asp Pro Asp Glu Glu Glu Asp Asp Glu Glu Glu Leu
135 1          5          10
137 Glu Glu Leu Glu Asp Ser Phe
138          15
142 (2) INFORMATION FOR SEQ ID NO: 5:
144     (i) SEQUENCE CHARACTERISTICS:
145         (A) LENGTH: 11 amino acids

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146          (B) TYPE: amino acid
147          (C) STRANDEDNESS: unknown
148          (D) TOPOLOGY: linear
150      (ii) MOLECULE TYPE: peptide
152      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
154      Asp Pro Asp Leu Glu Glu Leu Glu Asp Ser Phe
155      1          5          10
158 (2) INFORMATION FOR SEQ ID NO: 6:
160      (i) SEQUENCE CHARACTERISTICS:
161          (A) LENGTH: 223 base pairs
162          (B) TYPE: nucleic acid
163          (C) STRANDEDNESS: unknown
164          (D) TOPOLOGY: linear
166      (ii) MOLECULE TYPE: DNA (genomic)
168      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
171 GGATCCCCTT CCTACACAGC CTGCTGAAGA AGCAGCACGA          40
173 AAGAGAGAGG TTCGTCTAAT GAAGAACAGG GAAGCAGCAA          80
175 GAGAATGTCG TAGAAAGAAG AAAGAATATG TGAAATGTTT          120
177 AGAGAACAGA GTGGCAGTGC TTGAAAACCA AAACAAAACA          160
179 TTGATTGAGG AGCTAAAAGC ACTTAAGGAC CTTTACTGCC          200
181 ACAAGTCAGA TTAATTCAAG CTT          223
185 (2) INFORMATION FOR SEQ ID NO: 7:
187      (i) SEQUENCE CHARACTERISTICS:
188          (A) LENGTH: 68 amino acids
189          (B) TYPE: amino acid
190          (C) STRANDEDNESS: unknown
191          (D) TOPOLOGY: linear
193      (ii) MOLECULE TYPE: peptide
195      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
198 Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys
199 1          5          10
201 Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala
202 15          20
204 Arg Glu Cys Arg Arg Lys Lys Glu Tyr Val Lys
205 25          30          35
207 Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln
208 40          45
210 Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys
211 50          55          60
213 Asp Leu Tyr Cys His Lys Ser Asp
214 65
217 (2) INFORMATION FOR SEQ ID NO: 8:
219      (i) SEQUENCE CHARACTERISTICS:
220          (A) LENGTH: 290 base pairs
221          (B) TYPE: nucleic acid
222          (C) STRANDEDNESS: unknown
223          (D) TOPOLOGY: linear
226      (ii) MOLECULE TYPE: DNA (genomic)
228      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

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232 CCATGGACTA CAAGGACGAC GATGACAAGC ATATGGCTAG      40
234 CATGACTGGT GGACAGCAAA TGGGTCGGGA TCCCCTTCCT      80
236 ACACAGCCTG CTGAAGAAGC AGCACGAAAG AGAGAGGTTC     120
238 GTCTAATGAA GAACAGGGAA GCAGCAAGAG AATGTCGTAG     160
240 AAAGAAGAAA GAATATGTGA AATGTTTAGA GAACAGAGTG     200
242 GCAGTGCTTG AAAACCAAAA CAAAACATTG ATTGAGGAGC     240
244 TAAAAGCACT TAAGGACCTT TACTGCCACA AGTCAGATTA     280
246 ATTCAAGCTT                                290

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249 (2) INFORMATION FOR SEQ ID NO: 9:

251 (i) SEQUENCE CHARACTERISTICS:

252 (A) LENGTH: 92 amino acids

253 (B) TYPE: amino acid

254 (C) STRANDEDNESS: unknown

255 (D) TOPOLOGY: linear

257 (ii) MOLECULE TYPE: peptide

259 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

261 Met Asp Tyr Lys Asp Asp Asp Asp Lys His Met Ala

262 1 5 10

264 Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro

265 15 20

267 Leu Pro Thr Gln Pro Ala Glu Glu Ala Ala Arg Lys

268 25 30 35

270 Arg Glu Val Arg Leu Met Lys Asn Arg Glu Ala Ala

271 40 45

274 Arg Glu Cys Arg Arg Lys Lys Lys Glu Tyr Val Lys

275 50 55 60

277 Cys Leu Glu Asn Arg Val Ala Val Leu Glu Asn Gln

278 65 70

281 Asn Lys Thr Leu Ile Glu Glu Leu Lys Ala Leu Lys

282 75 80

284 Asp Leu Tyr Cys His Lys Ser Asp

285 85 90

288 (2) INFORMATION FOR SEQ ID NO: 10:

290 (i) SEQUENCE CHARACTERISTICS:

291 (A) LENGTH: 266 base pairs

292 (B) TYPE: nucleic acid

293 (C) STRANDEDNESS: unknown

294 (D) TOPOLOGY: linear

297 (ii) MOLECULE TYPE: DNA (genomic)

299 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

302 CCATGGACTA CAAGGACGAC GATGACAAGC ATATGGCTAG 40

304 CATGACTGGT GGACAGCAAA TGGGTCGGGA TCCTGACCTG 80

306 GAACAACGTG CTGAGGAACT GGCCCGTGAA AACGAAGAGC 120

308 TGGAAAAAGA GGCCGAAGAG CTGGAGCAGG AACTGGCAGA 160

310 ACTCGAGAAC AGAGTGGCAG TGCTTGAAAA CCAAAACAAA 200

312 ACATTGATTG AGGAGCTAAA AGCACTTAAG GACCTTTACT 240

314 GCCACAAGTC AGATTAATTC AAGCTT 266

317 (2) INFORMATION FOR SEQ ID NO: 11:

319 (i) SEQUENCE CHARACTERISTICS:

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/059,720

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Input Set : A:\PTO.AMC.txt

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320      (A) LENGTH: 84 amino acids
321      (B) TYPE: amino acid
322      (C) STRANDEDNESS: unknown
323      (D) TOPOLOGY: linear
325      (ii) MOLECULE TYPE: peptide
327      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
330 Met Asp Tyr Lys Asp Asp Asp Asp Lys His Met Ala
331 1      5      10
333 Ser Met Thr Gly Gly Gln Gln Met Gly Arg Asp Pro
334      15      20
336 Asp Leu Glu Gln Arg Ala Glu Glu Leu Ala Arg Glu
337 25      30      35
339 Asn Glu Glu Leu Glu Lys Glu Ala Glu Glu Leu Glu
340      40      45
342 Gln Glu Leu Ala Glu Leu Glu Asn Arg Val Ala Val
343      50      55      60
345 Leu Glu Asn Gln Asn Lys Thr Leu Ile Glu Glu Leu
346      65      70
348 Lys Ala Leu Lys Asp Leu Tyr Cys His Lys Ser Asp
349      75      80
352 (2) INFORMATION FOR SEQ ID NO: 12:
354      (i) SEQUENCE CHARACTERISTICS:
355          (A) LENGTH: 262 base pairs
356          (B) TYPE: nucleic acid
357          (C) STRANDEDNESS: unknown
358          (D) TOPOLOGY: linear
360      (ii) MOLECULE TYPE: DNA (genomic)
362      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
365 GGATCCCAAG GTGGAACAGT TATCTCCAGA AGAAGAAGAG      40
367 AAAAGGAGAA TCCGAAGGGA AAGGAATAAG ATGGCTGCAG      80
369 CCAAATGCCG CAACCGGAGG AGGGAGCTGA CTGATACACT      120
371 CCAAGCGGAG ACAGACCAAC TAGAAGATGA GAAGTCTGCT      160
373 TTGCAGACCG AGATTGCCAA CCTGCTGAAG GAGAAGGAAA      200
375 AACTAGAGTT CATCCTGGCA GCTCACCGAC CTGCCTGCAA      240
377 GATCCCTGAT TAATTCAAGC TT      262
379 (2) INFORMATION FOR SEQ ID NO: 13:
381      (i) SEQUENCE CHARACTERISTICS:
382          (A) LENGTH: 82 amino acids
383          (B) TYPE: amino acid
384          (C) STRANDEDNESS: unknown
385          (D) TOPOLOGY: linear
387      (ii) MOLECULE TYPE: peptide
389      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
392 Pro Asp Lys Val Glu Gln Leu Ser Pro Glu Glu Glu
393 1      5      10
395 Glu Lys Arg Arg Ile Arg Arg Glu Arg Asn Lys Met
396      15      20
398 Ala Ala Ala Lys Cys Arg Asn Arg Arg Arg Glu Leu
399 25      30      35

```

VERIFICATION SUMMARY

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L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]